SEQUENCE LISTING

<110> OTA, TOSHIO
ISOGAI, TAKAO
NISHIKAWA, TETSUO
HIO, YURI

<120> FULL LENGTH cDNA CLONES AND PROTEINS ENCODED THEREBY

<130> 084335-0155

<140> 10/031,589
<141> 2002-01-23

<150> PCT/JP00/04895
<151> 2000-07-21

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ggctcctagg gttcgggacg gtacgcacca gccaccttcg cgccgaaggc ggtagggcgc 180

cacggagagg aaccgctcta ggcacgtaag gcctcgtgag gttgcgtcgc gcgcggagca 240

ctctgggact tgtagttctg gag atg gag cga gct gtg ccg ctc gcg gtg cct 293
Met Glu Arg Ala Val Pro Leu Ala Val Pro
1 5 10

ctg ggt cag aca gag gtg ttc cag gcc ttg cag cgg ctc cat atg acc 341
Leu Gly Gln Thr Glu Val Phe Gln Ala Leu Gln Arg Leu His Met Thr
15 20 25

atc ttc tcc cag agc gtc tca cca tgt ggg aag ttt ctg gcg gct ggc 389
Ile Phe Ser Gln Ser Val Ser Pro Cys Gly Lys Phe Leu Ala Ala Gly
30 35 40

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aac aat tac ggg cag att gcc atc ttc agc ttg tcc tct gct ttg agc   437
Asn Asn Tyr Gly Gln Ile Ala Ile Phe Ser Leu Ser Ser Ala Leu Ser
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tca gaa gcc aaa gag gaa agt aag aag ccg gtg gtg act ttc caa gcc   485
Ser Glu Ala Lys Glu Glu Ser Lys Lys Pro Val Val Thr Phe Gln Ala
     60                  65                  70

cat gat ggg ccc gtc tat agc atg gtt tcc acc gat cga cat ctg ctt   533
His Asp Gly Pro Val Tyr Ser Met Val Ser Thr Asp Arg His Leu Leu
 75                  80                  85                  90

agt gct ggg gat ggg gag gag aag gcc tgg ctt tgg gcg gag atg ctc   581
Ser Ala Gly Asp Gly Glu Glu Lys Ala Trp Leu Trp Ala Glu Met Leu
                 95                 100                 105

aag aag ggc tgt aag gag ctg tgg cgt cgt cag cct cca tac agg acc   629
Lys Lys Gly Cys Lys Glu Leu Trp Arg Arg Gln Pro Pro Tyr Arg Thr
            110                 115                 120

agc ctg gaa gtg cct gag atc aac gct ttg ctg ctg gtc ccc aag gag   677
Ser Leu Glu Val Pro Glu Ile Asn Ala Leu Leu Leu Val Pro Lys Glu
        125                 130                 135

aat tcc ctc atc ctg gct ggg gga gac tgt cag ttg cac act atg gac   725
Asn Ser Leu Ile Leu Ala Gly Gly Asp Cys Gln Leu His Thr Met Asp
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ctt gaa act ggg act ttc acg agg gtc ctc cgg ggc cac aca gac tac   773
Leu Glu Thr Gly Thr Phe Thr Arg Val Leu Arg Gly His Thr Asp Tyr
155                 160                 165                 170

atc cac tgc ctg gca ctg cgg gaa agg agc cca gag gtg ctg tca ggt   821
Ile His Cys Leu Ala Leu Arg Glu Arg Ser Pro Glu Val Leu Ser Gly
                175                 180                 185

ggc gag gat gga gct gtt cga ctt tgg gac ctg cgc aca gcc aag gag   869
Gly Glu Asp Gly Ala Val Arg Leu Trp Asp Leu Arg Thr Ala Lys Glu
            190                 195                 200

gtc cag acg atc gag gtc tat aag cac gag gag tgc tcg agg ccc cac   917
Val Gln Thr Ile Glu Val Tyr Lys His Glu Glu Cys Ser Arg Pro His
        205                 210                 215

aat ggg cgc tgg att gga tgt ttg gca act gat tcc gac tgg atg gtc   965
Asn Gly Arg Trp Ile Gly Cys Leu Ala Thr Asp Ser Asp Trp Met Val
    220                 225                 230

tgt gga ggg ggc cca gcc ctc acc ctc tgg cac ctc cga tcc tcc aca   1013
Cys Gly Gly Gly Pro Ala Leu Thr Leu Trp His Leu Arg Ser Ser Thr
235                 240                 245                 250

ccc acc acc atc ttc ccc atc cgg gcg cca cag aag cac gtc acc ttc   1061
Pro Thr Thr Ile Phe Pro Ile Arg Ala Pro Gln Lys His Val Thr Phe
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tac cag gac ctg gtc ctg aca gct gca ggc aac agc tgc cgg gtg gat   1109
Tyr Gln Asp Leu Val Leu Thr Ala Ala Gly Asn Ser Cys Arg Val Asp
            270                 275                 280

gtc ttc acc aac ctg ggt tac cga gcc ttc tcc ctg tcc ttc           1151
Val Phe Thr Asn Leu Gly Tyr Arg Ala Phe Ser Leu Ser Phe
        285                 290                 295

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ttttttttt ttacaataaa gtttcaggct ttttt                            1246
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             20                  25                  30

Ser Pro Cys Gly Lys Phe Leu Ala Ala Gly Asn Asn Tyr Gly Gln Ile
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Ala Ile Phe Ser Leu Ser Ser Ala Leu Ser Ser Glu Ala Lys Glu Glu
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Ser Lys Lys Pro Val Val Thr Phe Gln Ala His Asp Gly Pro Val Tyr
 65                  70                  75                  80

Ser Met Val Ser Thr Asp Arg His Leu Leu Ser Ala Gly Asp Gly Glu
                 85                  90                  95

Glu Lys Ala Trp Leu Trp Ala Glu Met Leu Lys Lys Gly Cys Lys Glu
            100                 105                 110

Leu Trp Arg Arg Gln Pro Pro Tyr Arg Thr Ser Leu Glu Val Pro Glu
        115                 120                 125

Ile Asn Ala Leu Leu Leu Val Pro Lys Glu Asn Ser Leu Ile Leu Ala
    130                 135                 140

Gly Gly Asp Cys Gln Leu His Thr Met Asp Leu Glu Thr Gly Thr Phe
145                 150                 155                 160

Thr Arg Val Leu Arg Gly His Thr Asp Tyr Ile His Cys Leu Ala Leu
                165                 170                 175

Arg Glu Arg Ser Pro Glu Val Leu Ser Gly Gly Glu Asp Gly Ala Val
            180                 185                 190

Arg Leu Trp Asp Leu Arg Thr Ala Lys Glu Val Gln Thr Ile Glu Val
        195                 200                 205
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```
Tyr Lys His Glu Glu Cys Ser Arg Pro His Asn Gly Arg Trp Ile Gly
    210                 215                 220

Cys Leu Ala Thr Asp Ser Asp Trp Met Val Cys Gly Gly Gly Pro Ala
225                 230                 235                 240

Leu Thr Leu Trp His Leu Arg Ser Ser Thr Pro Thr Thr Ile Phe Pro
                245                 250                 255

Ile Arg Ala Pro Gln Lys His Val Thr Phe Tyr Gln Asp Leu Val Leu
            260                 265                 270

Thr Ala Ala Gly Asn Ser Cys Arg Val Asp Val Phe Thr Asn Leu Gly
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Tyr Arg Ala Phe Ser Leu Ser Phe
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tccccccatc cgcgggcgcg aatggtccgg gtcgcgtccg cagtgctgct ggctgctccc 180

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cacatgtgac ttcacctcag ttttgtgatc cgtaaaatgg acaaattcga agctacttca 540

cagtgctgtt gagaggatta aatgaaacaa tgcttgtaaa gctctttgca ggagggagcc 600

tcggaagcag ggcctggccg gcagagcaca cctgctgtca ccagggacca caggcagc   658

atg aag acc ccc gtg gag ctg gcc gtc agt ggg atg cag acc ctc ggc   706
Met Lys Thr Pro Val Glu Leu Ala Val Ser Gly Met Gln Thr Leu Gly
  1               5                  10                  15

ctt cag cac cgc tgc cga ggt ggc tac cgg gtc aag gcc agg acg tca   754
Leu Gln His Arg Cys Arg Gly Gly Tyr Arg Val Lys Ala Arg Thr Ser
             20                  25                  30
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tat gtg gat gag act ctg ttt ggc agc cca gca ggc acc cgg cct acc   802
Tyr Val Asp Glu Thr Leu Phe Gly Ser Pro Ala Gly Thr Arg Pro Thr
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cca ccg gac ttc gat ccg ccc tgg gtg gag aag gct aac aga acc aga   850
Pro Pro Asp Phe Asp Pro Pro Trp Val Glu Lys Ala Asn Arg Thr Arg
     50                  55                  60

ggc gtg ggc aag gag gca tcg aag gcc ttg ggg gca aag ggg agc tgt   898
Gly Val Gly Lys Glu Ala Ser Lys Ala Leu Gly Ala Lys Gly Ser Cys
 65                  70                  75                  80

gag acc acc ccc tca agg ggc agc acc ccc acc ctc aca cca agg aag   946
Glu Thr Thr Pro Ser Arg Gly Ser Thr Pro Thr Leu Thr Pro Arg Lys
                 85                  90                  95

aag aac aaa tac aga ccc atc agc cac acc ccg tct tac tgt gat gag   994
Lys Asn Lys Tyr Arg Pro Ile Ser His Thr Pro Ser Tyr Cys Asp Glu
            100                 105                 110

tcg ctg ttt ggc tcc cga tct gaa ggc gcc agc ttc ggg gcc ccg cgg   1042
Ser Leu Phe Gly Ser Arg Ser Glu Gly Ala Ser Phe Gly Ala Pro Arg
        115                 120                 125

atg gcg aag ggg gat gcc gca aag ctc cgt gct ctc ttg tgg acg cca   1090
Met Ala Lys Gly Asp Ala Ala Lys Leu Arg Ala Leu Leu Trp Thr Pro
    130                 135                 140

cca cct acc ccc agg ggt agc cac tcg ccc cgc ccc agg gag gca cca   1138
Pro Pro Thr Pro Arg Gly Ser His Ser Pro Arg Pro Arg Glu Ala Pro
145                 150                 155                 160

ctg cga gcc att cac cca gct ggt ccc tcc aag aca gag ccg ggg cca   1186
Leu Arg Ala Ile His Pro Ala Gly Pro Ser Lys Thr Glu Pro Gly Pro
                165                 170                 175

gcg gca gac tcc cag aag tta tct atg ggt ggg tta cac tct tca cgc   1234
Ala Ala Asp Ser Gln Lys Leu Ser Met Gly Gly Leu His Ser Ser Arg
            180                 185                 190

ccc ctg aag cgg gga ctt tcc cat tcc ctc acc cac ctg aat gtc ccc   1282
Pro Leu Lys Arg Gly Leu Ser His Ser Leu Thr His Leu Asn Val Pro
        195                 200                 205

agc act ggt cat cca gcc acc agt gcc ccc cac aca aat ggg cct cag   1330
Ser Thr Gly His Pro Ala Thr Ser Ala Pro His Thr Asn Gly Pro Gln
    210                 215                 220

gat ctc agg cct tcc acg tca ggg gtg acc ttc cgg agc ccc ctg gtg   1378
Asp Leu Arg Pro Ser Thr Ser Gly Val Thr Phe Arg Ser Pro Leu Val
225                 230                 235                 240

act tcc agg gct cgc tca gtt agc att tca gtg cca tct acc cca cga   1426
Thr Ser Arg Ala Arg Ser Val Ser Ile Ser Val Pro Ser Thr Pro Arg
                245                 250                 255
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cga ggt ggg gcc acc cag aaa cca aag ccc cct tgg aaa tgatactctt    1475
Arg Gly Gly Ala Thr Gln Lys Pro Lys Pro Pro Trp Lys
            260                 265

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cattcatcac ccagggaacc ccaggtatta aagaagcccc tgtgggggca gacagacata 1595

gcaggggtgg gcagtgcctc cctttatcct gacaatctct agtcgattct tgccttttc 1655

tcccgattgc ggatttgggg gccacctcta agatgcctct ctccagccct gtctcaacca 1715

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Tyr Val Asp Glu Thr Leu Phe Gly Ser Pro Ala Gly Thr Arg Pro Thr
         35                  40                  45

Pro Pro Asp Phe Asp Pro Pro Trp Val Glu Lys Ala Asn Arg Thr Arg
     50                  55                  60

Gly Val Gly Lys Glu Ala Ser Lys Ala Leu Gly Ala Lys Gly Ser Cys
 65                  70                  75                  80

Glu Thr Thr Pro Ser Arg Gly Ser Thr Pro Thr Leu Thr Pro Arg Lys
                 85                  90                  95

Lys Asn Lys Tyr Arg Pro Ile Ser His Thr Pro Ser Tyr Cys Asp Glu
            100                 105                 110

Ser Leu Phe Gly Ser Arg Ser Glu Gly Ala Ser Phe Gly Ala Pro Arg
        115                 120                 125

Met Ala Lys Gly Asp Ala Ala Lys Leu Arg Ala Leu Leu Trp Thr Pro
    130                 135                 140

Pro Pro Thr Pro Arg Gly Ser His Ser Pro Arg Pro Arg Glu Ala Pro
145                 150                 155                 160

Leu Arg Ala Ile His Pro Ala Gly Pro Ser Lys Thr Glu Pro Gly Pro
                165                 170                 175

Ala Ala Asp Ser Gln Lys Leu Ser Met Gly Gly Leu His Ser Ser Arg
            180                 185                 190
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Pro Leu Lys Arg Gly Leu Ser His Ser Leu Thr His Leu Asn Val Pro
        195                 200                 205

Ser Thr Gly His Pro Ala Thr Ser Ala Pro His Thr Asn Gly Pro Gln
    210                 215                 220

Asp Leu Arg Pro Ser Thr Ser Gly Val Thr Phe Arg Ser Pro Leu Val
225                 230                 235                 240

Thr Ser Arg Ala Arg Ser Val Ser Ile Ser Val Pro Ser Thr Pro Arg
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tccacaatct gggactcctc accaagccgg gtactctcct gcccaccgat aggaacaact 180

cc atg tgt acc acc atg cga gat aaa gtg ttt gga aat tac att cct    227
   Met Cys Thr Thr Met Arg Asp Lys Val Phe Gly Asn Tyr Ile Pro
     1               5                  10                  15

gtg cct gct act gac tgt atg gct gtt tca act ttc tgg att gct cat   275
Val Pro Ala Thr Asp Cys Met Ala Val Ser Thr Phe Trp Ile Ala His
                 20                  25                  30

ccc aac aat aat ctg att aat aat gca gct gca ggc tca cag gat gct   323
Pro Asn Asn Asn Leu Ile Asn Asn Ala Ala Ala Gly Ser Gln Asp Ala
             35                  40                  45

gga ata tgg tat tta ttc cac aag gaa cca act ggg gaa tcc agt gga   371
Gly Ile Trp Tyr Leu Phe His Lys Glu Pro Thr Gly Glu Ser Ser Gly
         50                  55                  60

ttg cag ctc ttg gca aaa cca gaa ctc act cca ttg ggt ata ttt tat   419
Leu Gln Leu Leu Ala Lys Pro Glu Leu Thr Pro Leu Gly Ile Phe Tyr
     65                  70                  75

aac aac agg gtc cat tca aat ttt aag gct ggc tta ttt att gac aaa   467
Asn Asn Arg Val His Ser Asn Phe Lys Ala Gly Leu Phe Ile Asp Lys
 80                  85                  90                  95
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ggt gtc aaa aca acc aac tct agt gct gct gac cca agg gaa tac ctc   515
Gly Val Lys Thr Thr Asn Ser Ser Ala Ala Asp Pro Arg Glu Tyr Leu
                100                 105                 110

tgt ttg gac aat agt gca aga ttt cga cct cat cag gat gca aac ccc   563
Cys Leu Asp Asn Ser Ala Arg Phe Arg Pro His Gln Asp Ala Asn Pro
            115                 120                 125

gaa aaa cca cgt gtt gct gct cta att gac agg ctc att gct ttt aaa   611
Glu Lys Pro Arg Val Ala Ala Leu Ile Asp Arg Leu Ile Ala Phe Lys
        130                 135                 140

aat aat gat aat gga gct tgg gtc aga gga gga gat att atc gtt caa   659
Asn Asn Asp Asn Gly Ala Trp Val Arg Gly Gly Asp Ile Ile Val Gln
    145                 150                 155

aat tca gca ttt gca gat aat gga ata gga ctg acc ttt gcc agt gat   707
Asn Ser Ala Phe Ala Asp Asn Gly Ile Gly Leu Thr Phe Ala Ser Asp
160                 165                 170                 175

gga agc ttc cca agt gat gaa ggt tcc agc caa gag gta tct gaa tct   755
Gly Ser Phe Pro Ser Asp Glu Gly Ser Ser Gln Glu Val Ser Glu Ser
                180                 185                 190

ctc ttt gtt ggg gag agc agg aat tac ggc ttt cag ggt ggt cag aac   803
Leu Phe Val Gly Glu Ser Arg Asn Tyr Gly Phe Gln Gly Gly Gln Asn
            195                 200                 205

aag tat gta ggc act gga gga ata gac cag aag cct cga aca tta ccc   851
Lys Tyr Val Gly Thr Gly Gly Ile Asp Gln Lys Pro Arg Thr Leu Pro
        210                 215                 220

agg aac agg acg ttc cca att aga ggc ttt cag att tat gat ggg ccc   899
Arg Asn Arg Thr Phe Pro Ile Arg Gly Phe Gln Ile Tyr Asp Gly Pro
    225                 230                 235

att cat ctc aca agg agc act ttc aaa aaa tat gtg cca act cca gat   947
Ile His Leu Thr Arg Ser Thr Phe Lys Lys Tyr Val Pro Thr Pro Asp
240                 245                 250                 255

agg tac agc agt gca att ggc ttc ctc atg aag aat tcc tgg cag ata   995
Arg Tyr Ser Ser Ala Ile Gly Phe Leu Met Lys Asn Ser Trp Gln Ile
                260                 265                 270

acc ccc agg aat aat atc tcc ctc gtg aag ttt ggt cca cat gtc tct  1043
Thr Pro Arg Asn Asn Ile Ser Leu Val Lys Phe Gly Pro His Val Ser
            275                 280                 285

ctg aat gtc ttt ttt gga aag cct ggt ccc tgg ttt gaa gat tgt gag  1091
Leu Asn Val Phe Phe Gly Lys Pro Gly Pro Trp Phe Glu Asp Cys Glu
        290                 295                 300

atg gat ggt gat aag aac tcc ata ttc cat gac att gat ggc tct gtg  1139
Met Asp Gly Asp Lys Asn Ser Ile Phe His Asp Ile Asp Gly Ser Val
    305                 310                 315
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aca gga tac aag gat gct tat gtg gga aga atg gac aac tac ctg atc   1187
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320                 325                 330                 335

cgc cat cca agc tgt gta aat gtg tct aag tgg aat gca gtg atc tgc   1235
Arg His Pro Ser Cys Val Asn Val Ser Lys Trp Asn Ala Val Ile Cys
                340                 345                 350

agt ggg acc tat gca cag gtc tat gta cag aca tgg agc act cag aat   1283
Ser Gly Thr Tyr Ala Gln Val Tyr Val Gln Thr Trp Ser Thr Gln Asn
            355                 360                 365

ctt tct atg acc att aca cga gat gag tat ccg tcc aac cct atg gtg   1331
Leu Ser Met Thr Ile Thr Arg Asp Glu Tyr Pro Ser Asn Pro Met Val
        370                 375                 380

ctc cga ggt att aat cag aag gct gcc ttt cca cag tac cag cct gtc   1379
Leu Arg Gly Ile Asn Gln Lys Ala Ala Phe Pro Gln Tyr Gln Pro Val
    385                 390                 395

gtc atg ctg gag aag ggt tat acc atc cac tgg aat ggg ccg gca cca   1427
Val Met Leu Glu Lys Gly Tyr Thr Ile His Trp Asn Gly Pro Ala Pro
400                 405                 410                 415

cgg act aca ttt cta tac ctc gtc aac ttc aac aag aat gac tgg att   1475
Arg Thr Thr Phe Leu Tyr Leu Val Asn Phe Asn Lys Asn Asp Trp Ile
                420                 425                 430

cga gtt ggc ctt tgc tat cca tca aac aca agt ttt caa gtt acc ttt   1523
Arg Val Gly Leu Cys Tyr Pro Ser Asn Thr Ser Phe Gln Val Thr Phe
            435                 440                 445

ggc tat ttg cag cgg cag aat ggc tca tta tcc aaa atc gaa gaa tat   1571
Gly Tyr Leu Gln Arg Gln Asn Gly Ser Leu Ser Lys Ile Glu Glu Tyr
        450                 455                 460

gag cct gtg cat tca ctg gaa gaa ctg caa aga aag caa tcc gag agg   1619
Glu Pro Val His Ser Leu Glu Glu Leu Gln Arg Lys Gln Ser Glu Arg
    465                 470                 475

aaa ttc tat ttt gac tcc agc acg ggg tta ctg ttt ttg tat ctc aaa   1667
Lys Phe Tyr Phe Asp Ser Ser Thr Gly Leu Leu Phe Leu Tyr Leu Lys
480                 485                 490                 495

gcc aaa agc cac agg cat ggc cac agt tac tgt tca tct cag gga tgt   1715
Ala Lys Ser His Arg His Gly His Ser Tyr Cys Ser Ser Gln Gly Cys
                500                 505                 510

gaa aga gtc aag atc caa gca gcc aca gac tca aag gac atc agt aac   1763
Glu Arg Val Lys Ile Gln Ala Ala Thr Asp Ser Lys Asp Ile Ser Asn
            515                 520                 525

tgc atg gcc aaa gca tac cca cag tac tac aga aag ccg tca gtg gtc   1811
Cys Met Ala Lys Ala Tyr Pro Gln Tyr Tyr Arg Lys Pro Ser Val Val
        530                 535                 540
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aag cgg atg ccg gcc atg ctc act gga ctc tgt caa ggc tgt ggc act   1859
Lys Arg Met Pro Ala Met Leu Thr Gly Leu Cys Gln Gly Cys Gly Thr
    545                 550                 555

cgg cag gtg gtg ttt act agt gat cct cat aaa agt tac ctc cct gtg   1907
Arg Gln Val Val Phe Thr Ser Asp Pro His Lys Ser Tyr Leu Pro Val
560                 565                 570                 575

caa ttc cag tca cct gat aaa gca gaa gcc cag cgt gga gac ccg tct   1955
Gln Phe Gln Ser Pro Asp Lys Ala Glu Ala Gln Arg Gly Asp Pro Ser
                580                 585                 590

gtt att tct gtc aat ggc act gac ttt acc ttc cga agt gca ggc gtc   2003
Val Ile Ser Val Asn Gly Thr Asp Phe Thr Phe Arg Ser Ala Gly Val
            595                 600                 605

ctc ctc ctt gtt gtg gat ccg tgc agc gtt cca ttc cgc ttg acg gaa   2051
Leu Leu Leu Val Val Asp Pro Cys Ser Val Pro Phe Arg Leu Thr Glu
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aaa acg gtt ttt cct ctt gct gat gtc agt cgc att gaa gag tat tta   2099
Lys Thr Val Phe Pro Leu Ala Asp Val Ser Arg Ile Glu Glu Tyr Leu
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aaa aca ggc atc cct cca agg tcc att gtt ctg ttg agc aca aga gga   2147
Lys Thr Gly Ile Pro Pro Arg Ser Ile Val Leu Leu Ser Thr Arg Gly
640                 645                 650                 655

gaa ata aag cag tta aac att tca cac tta cta gta cct ctg gga tta   2195
Glu Ile Lys Gln Leu Asn Ile Ser His Leu Leu Val Pro Leu Gly Leu
                660                 665                 670

gcc aaa cca gct cat ctt tat gac aaa ggg agt acc gta ttt ttg gga   2243
Ala Lys Pro Ala His Leu Tyr Asp Lys Gly Ser Thr Val Phe Leu Gly
            675                 680                 685

ttc agt gga aac ttt aaa cca tca tgg act aag cta ttt acc agt cct   2291
Phe Ser Gly Asn Phe Lys Pro Ser Trp Thr Lys Leu Phe Thr Ser Pro
        690                 695                 700

gct gga cag ggc ctt ggg gtg ctt gaa caa ttc ata cct ttg cag ctg   2339
Ala Gly Gln Gly Leu Gly Val Leu Glu Gln Phe Ile Pro Leu Gln Leu
    705                 710                 715

gac gaa tat ggt tgt ccc aga gcc acc act gtc cgc aga aga gac ctg   2387
Asp Glu Tyr Gly Cys Pro Arg Ala Thr Thr Val Arg Arg Arg Asp Leu
720                 725                 730                 735

gaa ctg cta aag caa gct tca aaa gca cat tagagactaa ctgtaactta     2437
Glu Leu Leu Lys Gln Ala Ser Lys Ala His
                740                 745

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ctatttttat tcacttatat atcaattact tgtaagggtt aaactttcaa acaggaagta 3037

tattgggaca aaagggctct tggggattag atatcccttt aatctgtgac cattgggcaa 3097

aaaattttcc tgcagcaaaa gtctgaggct gttgggacca tttttgcagc tttaatcctt 3157

agcctctttt gactgtatat ttgtgtttaa aatgcagagc tcaactgaat atttcctttt 3217

ttgttttgtt ttgttttgtt ttaagaagta ggttgttttc ctgaaccgta aacttgtatc 3277

attttaactt gcacaaagga agtctgttct tggtattgct cttgcacttg ggtttttgt 3337

tattgttttg tgtggatttt ttaaagcttt tctgttcacc ctcctgccag gaaaatccca 3397

gaaagcttaa tgatacccca aaatgattac acccagggag gaaaaaaagg agcgctttct 3457

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agtcactctt acttaatgaa atgttaaagc caattaaaaa gcatgctgtg atgcccagct 3577

tccctttcca cagggtgcat gcgtctcctg ctggtgaatc acatgcggca agaggcaact 3637

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acttggtttt tctgttttat atactaataa tcagggccta agttaaataa aaatatgtgt 4237

gcatgtattt t 4248

<210> 6
<211> 745
<212> PRT
<213> Homo sapiens

<400> 6

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Met Cys Thr Thr Met Arg Asp Lys Val Phe Gly Asn Tyr Ile Pro Val
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Pro Ala Thr Asp Cys Met Ala Val Ser Thr Phe Trp Ile Ala His Pro
             20                  25                  30

Asn Asn Asn Leu Ile Asn Asn Ala Ala Ala Gly Ser Gln Asp Ala Gly
         35                  40                  45

Ile Trp Tyr Leu Phe His Lys Glu Pro Thr Gly Glu Ser Ser Gly Leu
     50                  55                  60

Gln Leu Leu Ala Lys Pro Glu Leu Thr Pro Leu Gly Ile Phe Tyr Asn
 65                  70                  75                  80

Asn Arg Val His Ser Asn Phe Lys Ala Gly Leu Phe Ile Asp Lys Gly
                 85                  90                  95

Val Lys Thr Thr Asn Ser Ser Ala Ala Asp Pro Arg Glu Tyr Leu Cys
            100                 105                 110

Leu Asp Asn Ser Ala Arg Phe Arg Pro His Gln Asp Ala Asn Pro Glu
        115                 120                 125

Lys Pro Arg Val Ala Ala Leu Ile Asp Arg Leu Ile Ala Phe Lys Asn
    130                 135                 140

Asn Asp Asn Gly Ala Trp Val Arg Gly Gly Asp Ile Ile Val Gln Asn
145                 150                 155                 160

Ser Ala Phe Ala Asp Asn Gly Ile Gly Leu Thr Phe Ala Ser Asp Gly
                165                 170                 175

Ser Phe Pro Ser Asp Glu Gly Ser Ser Gln Glu Val Ser Glu Ser Leu
            180                 185                 190

Phe Val Gly Glu Ser Arg Asn Tyr Gly Phe Gln Gly Gly Gln Asn Lys
        195                 200                 205

Tyr Val Gly Thr Gly Gly Ile Asp Gln Lys Pro Arg Thr Leu Pro Arg
    210                 215                 220

Asn Arg Thr Phe Pro Ile Arg Gly Phe Gln Ile Tyr Asp Gly Pro Ile
225                 230                 235                 240

His Leu Thr Arg Ser Thr Phe Lys Lys Tyr Val Pro Thr Pro Asp Arg
                245                 250                 255

Tyr Ser Ser Ala Ile Gly Phe Leu Met Lys Asn Ser Trp Gln Ile Thr
            260                 265                 270
```

```
Pro Arg Asn Asn Ile Ser Leu Val Lys Phe Gly Pro His Val Ser Leu
        275                 280                 285

Asn Val Phe Phe Gly Lys Pro Gly Pro Trp Phe Glu Asp Cys Glu Met
    290                 295                 300

Asp Gly Asp Lys Asn Ser Ile Phe His Asp Ile Asp Gly Ser Val Thr
305                 310                 315                 320

Gly Tyr Lys Asp Ala Tyr Val Gly Arg Met Asp Asn Tyr Leu Ile Arg
                325                 330                 335

His Pro Ser Cys Val Asn Val Ser Lys Trp Asn Ala Val Ile Cys Ser
            340                 345                 350

Gly Thr Tyr Ala Gln Val Tyr Val Gln Thr Trp Ser Thr Gln Asn Leu
        355                 360                 365

Ser Met Thr Ile Thr Arg Asp Glu Tyr Pro Ser Asn Pro Met Val Leu
    370                 375                 380

Arg Gly Ile Asn Gln Lys Ala Ala Phe Pro Gln Tyr Gln Pro Val Val
385                 390                 395                 400

Met Leu Glu Lys Gly Tyr Thr Ile His Trp Asn Gly Pro Ala Pro Arg
                405                 410                 415

Thr Thr Phe Leu Tyr Leu Val Asn Phe Asn Lys Asn Asp Trp Ile Arg
            420                 425                 430

Val Gly Leu Cys Tyr Pro Ser Asn Thr Ser Phe Gln Val Thr Phe Gly
        435                 440                 445

Tyr Leu Gln Arg Gln Asn Gly Ser Leu Ser Lys Ile Glu Glu Tyr Glu
    450                 455                 460

Pro Val His Ser Leu Glu Glu Leu Gln Arg Lys Gln Ser Glu Arg Lys
465                 470                 475                 480

Phe Tyr Phe Asp Ser Ser Thr Gly Leu Leu Phe Leu Tyr Leu Lys Ala
                485                 490                 495

Lys Ser His Arg His Gly His Ser Tyr Cys Ser Ser Gln Gly Cys Glu
            500                 505                 510

Arg Val Lys Ile Gln Ala Ala Thr Asp Ser Lys Asp Ile Ser Asn Cys
        515                 520                 525

Met Ala Lys Ala Tyr Pro Gln Tyr Tyr Arg Lys Pro Ser Val Val Lys
    530                 535                 540

Arg Met Pro Ala Met Leu Thr Gly Leu Cys Gln Gly Cys Gly Thr Arg
545                 550                 555                 560

Gln Val Val Phe Thr Ser Asp Pro His Lys Ser Tyr Leu Pro Val Gln
                565                 570                 575
```

```
Phe Gln Ser Pro Asp Lys Ala Glu Ala Gln Arg Gly Asp Pro Ser Val
            580                 585                 590

Ile Ser Val Asn Gly Thr Asp Phe Thr Phe Arg Ser Ala Gly Val Leu
        595                 600                 605

Leu Leu Val Val Asp Pro Cys Ser Val Pro Phe Arg Leu Thr Glu Lys
    610                 615                 620

Thr Val Phe Pro Leu Ala Asp Val Ser Arg Ile Glu Glu Tyr Leu Lys
625                 630                 635                 640

Thr Gly Ile Pro Pro Arg Ser Ile Val Leu Leu Ser Thr Arg Gly Glu
                645                 650                 655

Ile Lys Gln Leu Asn Ile Ser His Leu Leu Val Pro Leu Gly Leu Ala
            660                 665                 670

Lys Pro Ala His Leu Tyr Asp Lys Gly Ser Thr Val Phe Leu Gly Phe
        675                 680                 685

Ser Gly Asn Phe Lys Pro Ser Trp Thr Lys Leu Phe Thr Ser Pro Ala
    690                 695                 700

Gly Gln Gly Leu Gly Val Leu Glu Gln Phe Ile Pro Leu Gln Leu Asp
705                 710                 715                 720

Glu Tyr Gly Cys Pro Arg Ala Thr Thr Val Arg Arg Arg Asp Leu Glu
                725                 730                 735

Leu Leu Lys Gln Ala Ser Lys Ala His
            740                 745
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<210> 7
<211> 1545
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (341)..(1006)

<400> 7

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gacacggctc ccaggcctct gacccctgct ctaattggga cctgctgtgt ggccctccct 180

tgcttaccag ctgacaggaa cccttcctca cccccaggtt ggacacgccg tttccaaggc 240

ctcatggctt ccttttttctt ggttactgcc tcgggctccc tgggagagat ctctttggtg 300

ccgaaaaccg gaacgggaag cctcagcacc ctggcccccc atg ccc ctc gtg ggg   355
                                              Met Pro Leu Val Gly
                                                1               5
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cag ggt ggg tat acc ctg tac acc ctc ctg gtt tgg gct gag ggc att   403
Gln Gly Gly Tyr Thr Leu Tyr Thr Leu Leu Val Trp Ala Glu Gly Ile
                 10                  15                  20

agg ggt acc ggg cgt ctt tgg ggt ggc att agc ccc cga gtt gct ttg   451
Arg Gly Thr Gly Arg Leu Trp Gly Gly Ile Ser Pro Arg Val Ala Leu
            25                  30                  35

gaa act gtc ata ctt tct tct gtc tta gaa ctc aga atc caa gaa atg   499
Glu Thr Val Ile Leu Ser Ser Val Leu Glu Leu Arg Ile Gln Glu Met
        40                  45                  50

gca tcc atg ggg ata ggc aac cag cca ttc atg gat gtc aag ccc aga   547
Ala Ser Met Gly Ile Gly Asn Gln Pro Phe Met Asp Val Lys Pro Arg
    55                  60                  65

gac cgg acc cct gac tgt gca gtg ata agc gac ggg gct ccc aaa tgt   595
Asp Arg Thr Pro Asp Cys Ala Val Ile Ser Asp Gly Ala Pro Lys Cys
70                  75                  80                  85

gca gtg atg agc gac cgg gtc ccc gac agc atc gtc aag ggc aca ggt   643
Ala Val Met Ser Asp Arg Val Pro Asp Ser Ile Val Lys Gly Thr Gly
                90                  95                 100

acg gtg gct cgg tcc cgc cct cac tca ccc tgc aga ggg cac tgg gcc   691
Thr Val Ala Arg Ser Arg Pro His Ser Pro Cys Arg Gly His Trp Ala
            105                 110                 115

tgt cat caa ggg cat ggg tac ggc ggc atc ggc ccc acc ctc act cgc   739
Cys His Gln Gly His Gly Tyr Gly Gly Ile Gly Pro Thr Leu Thr Arg
        120                 125                 130

cca cag agt gca cca ggc ctg tcg tca agg aca cgg gta cgg tgg cct   787
Pro Gln Ser Ala Pro Gly Leu Ser Ser Arg Thr Arg Val Arg Trp Pro
    135                 140                 145

cgg ccc cgc cct cac tca tcc tgc aga ggg cac tgg gcc agt ggc cga   835
Arg Pro Arg Pro His Ser Ser Cys Arg Gly His Trp Ala Ser Gly Arg
150                 155                 160                 165

cat ggt ggg ttg gat ggg cat gac tgc agt ggc aaa gcc tgg tcg gcc   883
His Gly Gly Leu Asp Gly His Asp Cys Ser Gly Lys Ala Trp Ser Ala
                170                 175                 180

ttt cag acg gct ctg atc cca ttc ccg aac ctg ggc tgc act tca gga   931
Phe Gln Thr Ala Leu Ile Pro Phe Pro Asn Leu Gly Cys Thr Ser Gly
            185                 190                 195

gcg gaa gcc agc ctg acg tgc ttt ctg tcc ctt tcc aga gtc aca aat   979
Ala Glu Ala Ser Leu Thr Cys Phe Leu Ser Leu Ser Arg Val Thr Asn
        200                 205                 210

gag agg gtc cac agc ggt gtc ctc ctc tgaccacgcc gccccttca         1026
Glu Arg Val His Ser Gly Val Leu Leu
    215                 220

agcgaccaca ctccaccatc tcagacagca gcacctcctc ttctagcagc cagtcctcct 1086
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ccatcctggg gtcgctgggc ctgcttgtgt cctccagccc agcccacccg ggcctatgga 1146

gccctgccca cagcccctgg tcatctgata tcagagcctg cgtcgaggaa gatgagccag 1206

agccagaact agagacgggc acccaggctg cagtgtgtga gggggctcct gctgtgctgc 1266

tgagccgcac acgccaggcc tgatgactgt cagggtggca gtgcccatca tgtggctaga 1326

acaatacaga gggagcagca cgccaggcct gatgactctg ggggtggcgg tgcccatcgc 1386

gtggctggaa cgatccagag ggaatagcac agcaggtgtc caggtatttc ccaggatttt 1446

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tccacttcca cccaagacaa cagcatagga aacagacct 1545

<210> 8
<211> 222
<212> PRT
<213> Homo sapiens

<400> 8

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Met Pro Leu Val Gly Gln Gly Gly Tyr Thr Leu Tyr Thr Leu Leu Val
  1               5                  10                  15

Trp Ala Glu Gly Ile Arg Gly Thr Gly Arg Leu Trp Gly Gly Ile Ser
             20                  25                  30

Pro Arg Val Ala Leu Glu Thr Val Ile Leu Ser Ser Val Leu Glu Leu
         35                  40                  45

Arg Ile Gln Glu Met Ala Ser Met Gly Ile Gly Asn Gln Pro Phe Met
     50                  55                  60

Asp Val Lys Pro Arg Asp Arg Thr Pro Asp Cys Ala Val Ile Ser Asp
 65                  70                  75                  80

Gly Ala Pro Lys Cys Ala Val Met Ser Asp Arg Val Pro Asp Ser Ile
                 85                  90                  95

Val Lys Gly Thr Gly Thr Val Ala Arg Ser Arg Pro His Ser Pro Cys
            100                 105                 110

Arg Gly His Trp Ala Cys His Gln Gly His Gly Tyr Gly Gly Ile Gly
        115                 120                 125

Pro Thr Leu Thr Arg Pro Gln Ser Ala Pro Gly Leu Ser Ser Arg Thr
    130                 135                 140

Arg Val Arg Trp Pro Arg Pro Arg Pro His Ser Ser Cys Arg Gly His
145                 150                 155                 160

Trp Ala Ser Gly Arg His Gly Gly Leu Asp Gly His Asp Cys Ser Gly
                165                 170                 175

Lys Ala Trp Ser Ala Phe Gln Thr Ala Leu Ile Pro Phe Pro Asn Leu
            180                 185                 190
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Gly Cys Thr Ser Gly Ala Glu Ala Ser Leu Thr Cys Phe Leu Ser Leu
195 200 205

Ser Arg Val Thr Asn Glu Arg Val His Ser Gly Val Leu Leu
210 215 220

<210> 9
<211> 30
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: An artificially synthesized oligo-cap linker sequence

<400> 9
agcaucgagu cggccuuguu ggccuacugg 30

<210> 10
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: An artificially synthesized oligo(dT) primer sequence

<400> 10
gcggctgaag acggcctatg tggccttttt ttttttttt tt 42

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: An artificially synthesized primer sequence

<400> 11
agcatcgagt cggccttgtt g 21

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: An artificially synthesized primer sequence

<400> 12
gcggctgaag acggcctatg t 21